19. An array as claimed in claim 17 or 110, wherein the different oligonucleotides constitute part or all of a complete set of oligonucleotides of a predetermined length.

20. An array as claimed in claim 17 or 110, wherein the entire nucleotide sequence of each oligonucleotide is predetermined.

21. An array as claimed in claim 17 or 110, wherein the oligonucleotides are attached at the different known locations using a computer-controlled application device.

22. An array as claimed in claim 21, wherein the computer-controlled application device includes an ink-jet printer or pen plotter.

23. An array as claimed in claim 17 or 110, wherein the oligonucleotides are between 8-20 nucleotides in length.

24. An array as claimed in claim 17 or 110, wherein the support is made of glass.

25. An array as claimed in claim 17 or 110, wherein the support is a glass microscopic slide.

26. An array of oligonucleotides for analysing mutations of a gene having a known nucleotide sequence, comprising a support having an impermeable surface to which are attached at different known locations a set of overlapping or partly overlapping or non-overlapping oligonucleotides which are complementary to a segment of the known nucleotide sequence of the gene.

27. An array as claimed in claim 26, wherein the gene is selected from the DMD, the HPRT, the Huntington's disease and the cystic fibrosis genes.

28. An array as claimed in claim 26, wherein the different locations are spaced apart by 10-100 um.

29. An array as claimed in claim 26, wherein the oligonucleotides have a predetermined length.

30. An array as claimed in claim 26, wherein the entire nucleotide sequence of each oligonucleotide of the set is predetermined.

31. An array as claimed in claim 26, wherein the oligonucleotides are attached at the different known locations using a computer-controlled application device.

32. An array as claimed in claim 31, wherein the computer-controlled application device includes an ink-jet printer or pen plotter.

33. An array as claimed in claim 26, wherein the oligonucleotides are between 8-20 nucleotides in length.

34. An array as claimed in claim 26, wherein the support is made of glass.

35. An array as claimed in claim 26, wherein the support is a glass microscopic slide.

~~36.~~ A method of making an array of oligonucleotides, which comprises:

attaching a plurality of oligonucleotides to an impermeable surface of a support, the oligonucleotides having different predetermined sequences and being attached at different known locations on the surface of the support through a computer-controlled printing device.

37. The method as claimed in claim 36 or 111, wherein the oligonucleotides are synthesized before attachment to the surface of the support.

38. The method as claimed in claim 36 or 111, wherein

the oligonucleotides are synthesized in situ on the surface of the support.

39. The method as claimed in claim 36 or 111, wherein the different known locations are spaced apart by 10-100 um.

40. The method as claimed in claim 36 or 111, wherein the different oligonucleotides constitute part or all of a complete set of oligonucleotides of a predetermined length.

41. The method as claimed in claim 36 or 111, wherein the entire nucleotide sequence of each oligonucleotide is predetermined.

42. The method as claimed in claim 38, wherein the oligonucleotides are attached at the different known locations using a computer-controlled application device.

43. The method as claimed in claim 36 or 111, wherein oligonucleotides are attached using an ink-jet printer or pen plotter.

44. The method as claimed in claim 36 or 111, wherein the oligonucleotides are between 8-20 nucleotides in length.

45. The method as claimed in claim 36 or 111, wherein the support is made of glass.

46. The method as claimed in claim 36 or 111, wherein the support is a glass microscopic slide.

~~47.~~ 3 A method for constructing an array of ~~oligomers~~ oligonucleotides of length s and composed of ~~n~~ different ~~monomers~~ nucleotides, which method comprises:

a) applying precursors for ~~n~~ different ~~monomers~~ the nucleotides separately to ~~n~~ a plurality of different regions of a surface,

b) applying precursors for ~~n~~ the different ~~monomers~~ nucleotides separately to ~~n~~ a plurality of different regions ~~within each of the n~~ amongst the plurality of different regions defined in a),

c) repeating the process ~~a total of s times~~ until each of said regions contains oligonucleotides of length s.

~~48.~~ 4 The method as claimed in claim ~~47~~ 3, wherein ~~the monomers are nucleotides and n is 4~~ the number of different nucleotides utilized is 4.

~~49.~~ 5 The method as claimed in claim ~~47~~ 3, where s is 8-20.

~~50.~~ 6 The method as claimed in claim ~~47~~ 3, wherein the regions are organized on the surface in rows and columns.

~~51.~~ 7 The method as claimed in claim ~~47~~ 3, wherein the precursors are applied through a computer-controlled printing device.

~~52.~~ 8 The method as claimed in claim ~~47~~ 3, wherein each region is ~~from 10 to~~ at least 100 microns wide.

53. The method as claimed in claim 47, wherein a solvent repellant grid is used to divide the surface or regions thereof into different regions.

~~54.~~ 9 A method of analysing a polynucleotide, which method comprises:

applying a labelled polynucleotide to be analysed or fragments thereof to an array of oligonucleotides under hybridisation conditions, wherein the array comprises a support having an impermeable surface to which a plurality of oligonucleotides having different predetermined sequences are attached to different known ~~cells~~ regions on the surface, and

analysing the polynucleotide by observing the ~~cells~~ regions where the polynucleotide or fragment thereof hybridizes and the ~~cells~~ regions where the polynucleotide or fragment thereof does not hybridize.

~~55.~~ 10 A method of comparing polynucleotide sequences,

which method comprises:

applying the polynucleotides to an array of oligonucleotides under hybridizing conditions, wherein the oligonucleotides have different predetermined sequences and are attached at different known locations on an impermeable surface of a support, and

observing the differences between the patterns of hybridisation.

56. The method as claimed in claim 55, which comprises an additional step of using the observed differences to design probes for sequences that differ between the polynucleotides.

57. The method as claimed in claim 55, wherein the polynucleotides are from a normal and a mutant organism.

58. The method as claimed in claim 55, wherein the polynucleotides are from cancer cells and their normal counterparts.

59. A method of reconstructing a polynucleotide sequence, by the use of an array of oligonucleotides immobilised on a surface of a support, which method comprises applying the polynucleotide to the array of oligonucleotides under hybridisation conditions:

a) finding a first oligonucleotide of the array of length s which gives a positive hybridisation signal,

b) examining the array for hybridisation to a second oligonucleotide the sequence of which overlaps the first oligonucleotide by s-1 bases,

c) optionally examining the array for hybridisation to a third oligonucleotide which overlaps the first oligonucleotide by a sequence of s-1 bases,

d) optionally continuing these steps so as to extend sequence information by one base in each direction at each step.

60. A method of analysing a polynucleotide, which method comprises:

a) providing a first array of all possible oligonucleotides of chosen length, s, such that applying the labelled polynucleotide to the array under hybridisation conditions results in about 5% labelled cells,

b) providing a second array consisting of oligonucleotides of length s+2 the sequences of which are those oligonucleotides that gave a positive signal in the previous step extended by one base in both directions, applying the polynucleotide to the second array under hybridizing conditions, and observing which oligonucleotides hybridize with the polynucleotide,

c) and optionally repeating step b) until no repeated

sequences are identified.

61. The method as claimed in claim 60, wherein the oligonucleotides of the second array are those oligonucleotides identified as repeats in step a), extended by one base in both directions.

62. The method as claimed in claim 54, 55 or 60, where the polynucleotide is amplified by the polymerase chain reaction.

63. The method as claimed in claim 62, wherein the polynucleotide is amplified from genomic DNA.

64. The method as claimed in claim 54, 55 or 60, wherein the polynucleotide is genomic DNA or messenger RNA population.

65. The method as claimed in claim 54, 55 or 60, wherein the polynucleotide is tagged with a fluorescent label.

66. The method as claimed in claim 54, 55 or 60, wherein the polynucleotide is radio-labelled and hybridisations on the array are detected by autoradiography.

67. The method as claimed in claim 66, wherein the digitizing scanner has a resolution of 1-125 um.

68. The method as claimed in claim 54, 55 or 60, wherein the oligonucleotides of the array constitute all or part of a complete set of oligonucleotides of defined length.

69. A method of analysing for a gene of known sequence, which method comprises providing an array of oligonucleotides comprising a support having an impermeable surface to which are attached at spaced locations a set of overlapping or partly overlapping or non-overlapping oligonucleotides complementary to the known sequence of the gene, applying the gene to the array under hybridisation conditions, and observing a pattern of hybridisation.

70. The method as claimed in claim 69, wherein the gene is selected from the DMD, the HRPT, the Huntington's disease and the cystic fibrosis genes.

71. A method for multiple sequence variants in multiple polynucleotides, which comprises:

a) laying down stripes of oligonucleotides corresponding to each sequence variant on the surface of a solid support,

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b) applying the polynucleotides to the surface under hybridisation conditions in stripes orthogonal to those of the oligonucleotides,

c) observing hybridisation at a site of intersection as an indication of the presence of a variant sequence in the polynucleotide.

72. A method of preparing a polynucleotide for hybridisation to an array of oligonucleotides of length s which method comprises:

a) degrading the polynucleotide to fragments of around s nucleotides by a method which produces random breakage,

b) labelling the fragments,

c) optionally isolating fragments of length s,

d) optionally using gel electrophoresis for c).

73. The method for analysing a polynucleotide according to claim 54, 55 or 60, which comprises using an array of oligonucleotides segregated such that the different regions have different base compositions to compensate for the differences in stability of duplexes of differing base composition.

74. The method as claimed in claim 73, in which array is further segregated during hybridisation so that each area is

exposed to different hybridisation conditions.

75. A method for determining the sequence of a polynucleotide, which comprises:

applying the polynucleotide to a substrate having an impermeable surface to which are immobilise a plurality of oligonucleotide probes having different predetermined sequences under hybridisation conditions, wherein the probes are immobilised at different known locations on the surface of the support,

detecting the oligonucleotide probes to which the polynucleotide hybridizes, and

determining the sequence of the polynucleotide based upon the known sequence of the oligonucleotide probe to which the polynucleotide hybridizes.

76. The method according to claim 75, wherein the polynucleotide is labelled.

77. The method according to claim 75, wherein a plurality of polynucleotides are applied to the substrate.

78. The method according to claim 77, wherein the plurality of polynucleotides are fragments of a gene.

79. The method as claimed in claims 54, 55 or 60 wherein the polynucleotide is applied to the array under hybridisation conditions in the presence of a quaternary or tertiary amine.

80. The method as claimed in claim 79, wherein the amine is tetraethylammonium chloride used at a concentration in the range 2M to 5.5M.

81. The method as claimed in claim 54, 55 or 60, wherein for analysing a polynucleotide of length N, there is used an array of oligonucleotides of length s, where 4^s is an order of magnitude greater than N.

82. A method of making an array of oligonucleotides, which method comprises forming a solvent repellant grid on an impermeable surface of a support, said solvent repellant grid having exposed regions and building the oligonucleotides on the exposed regions.

83. A method of making an oligonucleotide array, which method comprises sintering microporous glass in microscopic patches on to the surface of the glass plate and providing oligonucleotides on said microscopic patches of microporous glass.

84. The array as claimed in claim 17, for probing many different mutations simultaneously, wherein stripes of oligonucleotides are present corresponding to allelic variants to be probed.

85. The array as claimed in claim 84, wherein the support carries at least one oligonucleotide stripe per mm.

~~86~~ 2. The method as claimed in claim ~~36~~ 1, wherein stripes of oligonucleotides, corresponding to allelic variants of a polynucleotide to be probed, are attached to the impermeable surface of the support.

87. The method as claimed in claim 86, wherein at least one oligonucleotide stripe is attached per mm of the support.

88. The method as claimed in claim 71, wherein the stripes of oligonucleotides have a width of 1 mm or less and the polynucleotides are applied in orthogonal stripes about 5 mm wide.

89. A method as claimed in claim 54, 59 or 60, wherein the oligonucleotides of the array are present in excess over the polynucleotide, so as to distinguish between hybridisations

involving single and multiple occurrences of a polynucleotide sequence.

90. The method as claimed in claim 54, 55 or 60, wherein the polynucleotide is DNA or RNA.

91. The method as claimed in claim 54, 55 or 60, wherein the hybridisation temperature is chosen to be close to the Tm of duplexes and is controlled to better than 0.5°C.

92. The method of claim 36 or 47, wherein the amount of an oligonucleotide attached on the surface of the support is dependant on its nucleotide composition.

93. The method of claim 54 or 60, wherein the analysis is performed by a computer programmed to compensate for variations in nucleotide composition.

94. The method of claim 54, 55 or 60, wherein hybridisations are detected by means of a digitising scanner.

Sub D2

95. The array of claim 17, wherein the oligonucleotides are attached in square or rectangular patches on the surface of the support.

96. A method of making an array of oligonucleotides, which method comprises a) applying a mask to an impermeable surface of a support thereby to define a first exposed region of the surface to which a first nucleotide residue is coupled, b) off-setting the mask thereby to define a second exposed region of the surface to which a second nucleotide residue is coupled, and c) repeating step b) until the desired array of oligonucleotides has been made.

97. The method of claim 43, wherein the pen plotter includes a component carrying a polytetrafluoroethylene tube.

98. The method claim 43, wherein the pen plotter is moved into position and the pen is lowered to lay down a coupling solution.

99. The method of claim 98, wherein the pen is filled successfully with different nucleotide precursor solutions so as to lay down oligonucleotides in groups in which oligonucleotides differ by single nucleotide residues.

100. The array of claim 17, wherein the oligonucleotides are arranged in groups in which oligonucleotides differ by single nucleotide residues.

101. The array of claim 17, wherein pairs of oligonucleotides represent allelic polymorphisms.

102. The array of claim 101, wherein at least 50 pairs of oligonucleotides are present.

103. The method of claim 96, wherein the mask is of silicone rubber.

104. The array of claim 17, wherein one part of each oligonucleotide has a predetermined sequence and another part is made up of all possible sequences.

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105. The array of claim 17, wherein each oligonucleotide has the sequence N_mAATAAAN$_n$ or its complement where N is any nucleotide residue and m+n is at least about 8.

106. The array as claimed in claim 17, wherein the oligonucleotides having different nucleotide sequences are attached from 72 to 10^4 different locations on the surface of the support.

107. The array as claimed in claim 17 or claim 26, wherein each oligonucleotide is attached by a covalent link through a terminal nucleotide residue on the surface of the

support.

108. The method of claim 36, wherein the oligonucleotides having different nucleotide sequences are attached at from 72-10^{12} different locations on the surface of the support.

109. The method of claim 36, wherein each oligonucleotide is attached by a covalent link through a terminal nucleotide residue on the surface of the support.

110. An array of oligonucleotides comprising a support having a surface to which the oligonucleotides are attached, wherein oligonucleotides having different nucleotide sequences are attached at between 72 and 10^{12} different known locations on the surface of the support.

111. A method of making an array of oligonucleotides, which comprises attaching oligonucleotides to a surface of a support, the oligonucleotides having different predetermined sequences and the oligonucleotides being attached at between 72 and 10^{12} different known locations on the surface of the support.

112. The array of claim 17 or claim 110 wherein, for analysing a polynucleotide of length N, the oligonucleotides of